

Interactive Loupe Files for 10x Genomics Projects

.cloupe and .loupe deliverables from Cell Ranger, Cell Ranger ARC, and Space Ranger

Overview

As part of our 10x Genomics standard data processing, the MU Genomics Technology Core now provides interactive visualization files that let you explore your single-cell, single-nucleus, and spatial datasets with no command-line or programming experience. These files open in Loupe Browser, a free desktop application from 10x Genomics available for Windows and macOS. Once we deliver the file, the full processed dataset travels with it and can be explored on your own laptop.

What These Files Are

.cloupe files are produced by Cell Ranger (count and multi), Cell Ranger ARC (Multiome), and the immune-profiling pipelines. They package the feature-barcode matrix, dimensionality reductions, and clustering into a single portable file.

.loupe files are produced by Space Ranger for Visium Spatial Gene Expression and additionally embed the tissue image with spot/barcode coordinates registered to it.

Both are self-contained. There is nothing to install beyond Loupe Browser itself, and no separate data files are required to open and explore them.

What the Files Contain

Depending on assay type, a delivered file may include:

- **Feature-barcode expression matrix** — normalized gene/feature counts per cell, nucleus, or spot.
- **Precomputed dimensionality reductions** — UMAP and t-SNE projections.
- **Automated clustering** — graph-based and K-means clusters at multiple resolutions.
- **Differential expression** — genes distinguishing each cluster, precomputed and searchable.
- **Spatial registration (Visium)** — expression overlaid on the H&E or fluorescence tissue image.
- **ATAC peaks and accessibility (ARC Multiome)** — chromatin accessibility alongside paired gene expression.
- **V(D)J clonotypes (Immune Profiling)** — clonotype grouping linked to expression clusters in Loupe V(D)J Browser.

What You Can Do With Them

Loupe Browser is a point-and-click environment for exploring results interactively:

- Visualize cells or spots on UMAP, t-SNE, or the tissue image, and color by gene expression, cluster, or metadata.
- Identify cell populations by exploring marker gene expression in real time.
- Create custom groupings and run differential expression between any cell sets you define.
- Search for specific genes or features and see where they are expressed.
- Rename, merge, and annotate clusters to build biologically meaningful cell-type labels.
- Export figures, gene lists, and coordinate tables for publications and downstream analysis.

Example Views by Project Type

The view types most relevant to each supported assay are described below. The **Official 10x Genomics Reference Pages** table that follows links to the vendor tutorials demonstrating each of these views.

Single-Cell / Single-Nucleus Gene Expression (3' and 5', GEM-X and prior)

UMAP or t-SNE projections colored by graph-based clusters, with feature plots showing marker gene expression per cell. Clusters can be reclustered, filtered on QC metrics, renamed, and annotated to cell types.

Visium Spatial Gene Expression

Gene expression overlaid on the registered H&E or fluorescence tissue image, showing spatial expression patterns across the section alongside the barcode/spot coordinates.

Single-Cell ATAC and Multiome (ARC)

Chromatin accessibility projections alongside paired gene expression, with peak and gene-activity views for jointly profiled nuclei.

Single-Cell Immune Profiling — V(D)J

Clonotype groupings visualized in Loupe V(D)J Browser and integrated with gene-expression clusters from the paired 5' library.

Official 10x Genomics Reference Pages

These links point to the vendor tutorials that demonstrate each view type. Use them as a reference for what each visualization looks like, or to direct clients to source documentation.

Assay / view	Where it appears in Loupe	Official 10x reference
Loupe Browser — navigation & UMAP/t-SNE	Interface, projections, split view, export	Loupe navigation tutorial
Single-Cell Gene Expression & Flex	Clustering, DE, sharing via .cloupe	Gene Expression tutorials
Public PBMC scRNA-seq walkthrough	UMAP, reclustering, cell-type annotation	PBMC analysis tutorial
Filtering & reanalysis	QC filtering, new projections in .cloupe	Reanalysis workflow
Immune Profiling — V(D)J	Integrated V(D)J + gene expression	Immune Profiling tutorial

Why This Adds Value

A .cloupe or .loupe file bridges the gap between raw sequencing output and biological insight. It puts a publication-grade, point-and-click exploration tool directly in the hands of investigators — no bioinformatics support required to begin interpreting results, generating hypotheses, and identifying cell populations of interest before committing to deeper custom analysis.